SEQUENCE LISTING

<110> KYOWA HAKKO KOGYO CO., LTD.

<120> Protein-free medium adapted FUT8 knouck out cells

<130> 11620W01.

<150> JP2003-350166

<151> 2003-10-09

<160> 32

<170> PatentIn Ver. 2.1

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<211> 2008

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<211> 3677

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<212> PRT

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170

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175

165

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185

190

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<212> PRT

<213 Homo sapiens

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Ser Ile Met Thr Asp Leu Tyr Tyr Leu Ser Gln Thr Asp Gly Ala Gly 35 40 45

Asp Trp Arg Glu Lys Glu Ala Lys Asp Leu Thr Glu Leu Val Gln Arg 50 55 60

Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys Lys 165 70 75 80

Leu Val Cys Asn Ile Asn Lys Gly Cys Gly Tyr Gly Cys Gln Leu His
85 90 95

His Val Val Tyr Cys Phe Met Ile Ala Tyr Gly Thr Gln Arg Thr Leu 100 105 110

Ile	Leu	Glu 115	Ser	Gln	Asn	Trp	Arg 120	Tyr	Ala.	Thr	Gly	Gly 125.	Trp	Glu	Thr
Val	Phe 130	Arg	Pro	Val	Ser	Glu 135	Thr	Cys	Thr	Asp	Arg. 140	Ser	Gly	Ile	Ser
Thr 145	Gly	His	Trp	Ser	Gly 150	Glu	Val	Lys	Asp	Lys 155	Asn	Va ⁻ l	Gln	Val	Va l
Glu	Leu	Pro	Ile	Val 165	Asp	Ser	Leu	His	Pro 170		Pro	Pro	Tyr	Leu 175	Pro
Leu	Ala	Val	Pro 180	Glu	Asp	Leu	Ala	Asp 185	Arg	Leu	Val	Arg	Val 190	His	Gly
Asp	Pro	Ala 195		Trp	Trp	Val	Ser 200	Gln	Phe	Val.	Lys	Tyr 205	Leu	Ile	Arg
Pro	Gln 210	Pro	Trp	Leu	Glu	Lys 215		Ile	Glu	Glu	Ala 220	Thr	Lys	Lys	Leu
Gly 225	Phe	Lys	His	Pro	Val ⁻ 230	Ile	Gly	Val	His	Val 235	Arg	Arg	Thr	Asp	Lys 240
Val	Gly	Thr	Glu	Ala 245	Ala-	Phe	His.		Ile 250	Glu.	Glu	Tyr	Met	Val 255	His
Val	Glu	Glu	His 260	Phe	Gln	Leu	Leu	Ala 265	Arg	Arg	Met	Gln	Val 270	Asp	Lys
Lys	Arg	Val	Tyr	Leu	Ala	Thr	Asp	Asp	Pro	Ser	Leu	Leu	Lvs	Glu	Ala

Lys Thr Lys Tyr Pro Asn Tyr Glu Phe Ile Ser Asp Asn Ser Ile Ser

Trp Ser Ala Gly Leu His Asn Arg Tyr Thr Glu Asn Ser Leu Arg Gly 305 310 315 320

Val Ile Leu Asp Ile His Phe Leu Ser Gln Ala Asp Phe Leu Val Cys 325 330 335

Thr Phe Ser Ser Gln Val Cys Arg Val Ala Tyr Glu Ile Met Gln Thr 340 345 350

Leu His Pro Asp Ala Ser Ala Asn Phe His Ser Leu Asp Asp Ile Tyr 355 360 365

Tyr Phe Gly Gly Gln Asn Ala His Asn Gln Ile Ala Ile Tyr Ala His 370 375 380

Gln Pro Arg Thr Ala Asp Glu Ile Pro Met Glu Pro Gly Asp Ile Ile 385 390 395 400

Gly Val Ala Gly Asn His Trp Asp Gly Tyr Ser Lys Gly Val Asn Arg 405 410 415

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Ile Glu Thr Val Lys Tyr Pro Thr Tyr Pro Glu Ala Glu Lys
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<212> PRT

<213> Sus scrofa

<400> 8

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Asn	Asp	His 35	Ser	.Asp	His	Ser	Ser 40		Glu	Leu	Ser	Lys 45	Ile	Leu	Ala
Lys	Leu 50	Glu	Arg	Leu	Lys	Gln 55	Gln	Asn	Glu	Asp	Leu 60	Arg	Arg	Met	Alà
Glu 165	Ser	Leu	Arg	Ile	Pro 70	Glu	Gly	Pro	Ile	Asp 75	Gln	Gly	Pro	Ala	Ser 80
Gly	Arg	Val	Arg	Ala 85	Leu	Glu	Glu	Gln	Phe 90	Met	Lys	Ala	Lys	Glu 95	Gln
Ile	Glu	Asn	Tyr 100	L.ys	Lys	Gln	Thr	Lys 105	Asn	Gly	Pro	Gly	Lys 110	Asp	His
Glu	Ile	Leu 115	Arg	Arg	Arg	Ile	Glu 120	Asn	Gly	Ala	Lys	Glu 125	Leu	Trp	Phe
Phe	Leu 130	Gln	Ser	Glu	Leu	Lys 135	Lys	Leu	Lys	Asn	Leu 140	Glu	Gly	Asn	Glu
Leu 145	Gln	Arg	His	Ala	Asp 150	Glu	Phe	Leu	Ser	Asp 155	Leu	Gly	His	His	Glu 160
Arg	Ser	Ile.	Met	Thr 165	Asp	Leu	Tyr		Leu 170	Ser	Gln	Thr	Asp	Gly 175	
Gly	Asp	Trp	Arg 180	Glu	Lys	Glu	Ala	Lys 185	Asp	Leu	Thr	Glu	Leu 190	Val	Gln

Arg Arg Ile Thr Tyr Leu Gln Asn Pro Lys Asp Cys Ser Lys Ala Lys

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His 225	His	Val	Val	Tyr	Cys 230	Phe	Met	Ile	Ala	Tyr 235	Gly	Thr	Gln	Arg	Thr 240
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Val	Glu 290	Leu	Pro	Ile	Val	Asp 295	Ser	Val	His	Pro	Arg 300	Pro	Pro	Tyr	Lėu
Pro 305	Leu	Ala	Val	Pro	Glu 310	Asp	Leu	Ala	Asp	Arg 315	Leu	Val	Arg	Val	His
Gly	Asp	Pro	Ala	Val 325	Trp	Trp	Val	Ser	Gln 330	Phe	Val	Lys	Tyr	Leu 335	Ile
Arg	Pro	.Gln	Pro 340	Trp	Leu	Glu	Lys	Glu 345	Ile	Glu	Glu	Ala	Thr 350	Lys	Lys
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Lys	Val 370	Gly	Ala	Glu	Ala	Ala 375	Phe	His	Pro-	Ile	Glu 380	Glu	Tyr	Thr	Val

His Val Glu Glu Asp Phe Gln Leu Leu Ala Arg Arg Met Gln Val Asp

385					390					395					400
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Ala	Lys	Thr	Lys 420	Tyr	Pro	Ser	Tyr	Glu 425		Ile	Ser	Asp	Asn 430	Ser	Ile
Ser	Trp	Ser 435	Ala	Gly	Leu	His	Asn 440	Arg	Tyr	Thr	Glu	Asn 445	Ser	Leu	Arg
Gly	Val 450	Ile	Leu	Asp	Ile	His 455	Phe	Leu	Ser	Gln	Ala 460	Asp	Phe	Leu	.Val
Cys 465	Thr	Phe	Ser	Ser	Gln 470	Val	Cys	Arg	Val	Ala 475	Tyr	Glu	Ile [°]	Met	Gln 480
Ala	Leu	His	Pro	Asp 485	Ala	Ser	Ala	Asn	Phe 490	Arg	Ser	Leu	Asp	Asp 495	Ile
Tyr	Tyr	Phe	Gly 500	Gly	Pro	Asn	Ala	His 505	Asn	Gln	Ile	Ala	Ile 510	Tyr	Pro
His	Gln	Pro- 515	Arg	Thr	Glu	Gly	Glu 520	Ile	Pro	Met	Glu	Pro 525	Gly	Asp	Ile
Ile	Gly 530	Val	Ala	Gly	Asn	His 535	Trp	Asp	Gly		Pro .540	Lys	Gly	Val	Asn
Arg 545		Leu	Gly	Arg	Thr 550	Gly	Leu	Tyr	Pro	Ser 555	Tyr	Lys	Val	Arg	Glu 560
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<211> 9196

<212> DNA

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4004																
<220			: 4 ; ,		£ 1	. : • : .	.:.1	Coar		· · · · · ·	4 l	.4:.	TO NI A			
\446	וע קנ	escri	ipiid	. 110	I AF	1111	STAT	Seqi	uence	s: ' 27	/ntne	eiic	DNA			
<400)> 1'	7 .														
ccts	gact	tgg (ctat	tctc	ag			٠								20
			•	•									•			
														•		
-)> 1															
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₹213	3> MI	us mi	ıscu	ıus												
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Met	Asp	Phe	Gln	Val	Gln	Ile	Ile	Ser	Phe	Leu	Leu	Ile	Şer	Ala	Ser	
1				5					10				•	15		
gtc	ata	atg	tcc	aga	gga	caa	a t t	gtt	ctc	tcc	cag	tc.t	cca	gca	atc	96
Val	Ile	Met	Ser	Arg	Gly	Gln	Ile	Val	Leu	Ser	Gln	Ser	Pro	Ala	Ile	•
			20			•		25					30			
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Leu	Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Arg	Ala	Ser	
	•	35			-		40					45				
		gta							_	_	_					192
Ser		Val	Ser	Tyr	Ile	His	Trp	Phe	Gln	Gln	Гл'n	Pro	Gly	Ser	Ser	
	50					55		•			60					•
		ccc														240
	Lys	Pro	Trp	Ile.		Ala	Thr	Ser	Asn		Ala	Ser	Gly	Val.	Pro	•
65					70					75					80	

gtt cgc ttc ag	t ggc agt ggg	tct ggg act	tct tac tct	ctc acc ato	288
Val Arg Phe Se	r Gly Ser Gly	Ser Gly Thr	Ser Tyr Ser	Leu Thr Ile	9
	85	90		95	
agc aga gtg ga	g gct gaa gat	gct gcc act	tat tac tgc	cag cag tgg	g 336
Ser Arg Val Gl	u Ala Glu Asp	Ala Ala Thr	Tyr Tyr Cys	Gln Gln Tr)
10	0.	105		110	
act agt aac cc	a ccc acg ttc	gga ggg ggg	acc aag ctg	gaa atc aas	a 384
Thr Ser Asn Pr	o Pro Thr Phe	Gly Gly Gly	Thr Lys Leu	Glu Ile Lys	3
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Val Leu Ser Gl			Gly Ala Glu		3
2		25		30	
cct ggg gcc tc			•		
Pro Gly Ala Se	r val Lys Met			Tyr Thr Phe	9
35		40	45		. 100
acc agt tac aa			•	•	
Thr Ser Tyr As		val Lys Gin		Arg Gly Let	I
50	55	222 992 224	60	.	0.40
gaa tgg att gg					
Glu Trp Ile Gl		Pro Gry Asii			
65	70	ana tta nat	75	. 80	
.cag aag ttc aa		•		•	
Gln Lys Phe Ly	•	•	AIA ASP LYS		
000 000 100 01	85	90	tot ~~~	95	
aca gcc tac at	g cag cic ago	age cig aca	ici gag gac	ici gcg gto	336

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val	
tat tac tgt gca aga tcg act tac tac ggc ggt gac tgg tac ttc aat	384
Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn	001
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